Table S1. PROCHECK analysis of homology-modeled SLH domains from *Bacillus anthracis*

| Polypeptide | | PROCHECK allowed regions (non Gly/Pro residues) | | | | | |
NCBI locus	Name	Identity/ similarity[a]	Most (A, B, L)	Additional (a, b, l, p)	Generous (~a, b, l, p)	Disallowed	G-factor[b]
BAS0841	Sap	-	138 (92%)	12 (8%)	0	0	0.17
BAS0842	EA1	59/75	143 (94.7%)	8 (5.3%)	0	0	0.05
pXO1-90	BslA	28/46	145 (86.6%)	18 (10.7%)	3 (1.8%)	2 (1.2%)	-0.13
pXO1-54	BslB	34/52	137 (89%)	14 (9.1%)	2 (1.3%)	1 (0.6%)	-0.12
BAS0916	BslC	28/45	146 (90.1%)	13 (8.0%)	1 (0.6%)	2 (1.2%)	-0.04
BAS1048	BslD	33/51	140 (90.3%)	12 (7.7%)	1 (0.6%)	2 (1.3%)	-0.09
BAS1049	BslE	30/48	136 (87.2%)	18 (11.5%)	1 (0.6%)	1 (0.6%)	-0.06
BAS1050	BslF	29/46	130 (86.1%)	19 (12.6%)	1 (0.7%)	1 (0.7%)	-0.13
BAS1787	BslG	30/49	140 (90.3%)	14 (9.0%)	0	1 (0.6%)	-0.07
BAS2160	BslH	35/53	139 (91.4%)	13 (8.6%)	0	0	-0.06
BAS3093	BslI	33/49	144 (91.1%)	12 (7.6%)	2 (1.3%)	0	-0.1
BAS3425	BslJ	30/48	139 (87.4%)	17 (10.7%)	3 (1.9%)	0	-0.1
BAS1021	BslK	52/67	144 (92.3%)	8 (5.1%)	3 (1.9%)	1 (0.6%)	-0.05
BAS1246	BslL	33/55	140 (92.7%)	10 (6.6%)	0	1 (0.7%)	0
BAS2613	BslM	28/50	141 (86.0 %)	23 (14.0%)	0	0	-0.2
BAS4693	BslN	27/45	138 (90.2%)	14 (9.2%)	0	1 (0.7%)	-0.04
BAS1683	BslO	34/50	144 (92.3%)	10 (6.4%)	2 (1.3%)	0	-0.07
BAS0829	BslP	28/44	140 (88.1%)	15 (9.4%)	3 (1.9%)	1 (0.6%)	-0.12
BAS3089	BslQ	26/43	143 (89.9%)	12 (7.5%)	3 (1.9%)	1 (0.6%)	-0.07
BAS3463	BslR	28/48	137 (90.7%)	11 (7.3%)	1 (0.7%)	2 (1.3%)	-0.05
BAS0851	BslS	55/69	136 (91.9%)	9 (6.1%)	1 (0.7%)	2 (1.4%)	-0.04
BAS1682	BslT	86/92	143 (93.5%)	10 (6.5%)	0	0	-0.06
BAS2351	BslU	53/68	137 (89.5%)	13 (8.5%)	3 (2.0%)	0	-0.05
pXO2-42	AmiA	55/71	139 (93.3%)	8 (5.4%)	1 (0.7%)	1 (0.7%)	-0.03

[a]Peptide sequence identity / similarity in percent (%) as compared to *B. anthracis* Sap.
[b] The overall average of the G-factor is indicated.